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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,118

DATE: 05/02/2001

TIME: 12:11:46

Input Set : A:\PF544SL.txt

Output Set: N:\CRF3\05022001\I833118.raw

P.S

ENTERED

C--> 3 <110> APPLICANT: Rosen, Craig A.
4 Haseltine, William A.
6 <120> TITLE OF INVENTION: Albumin Fusion Proteins
8 <130> FILE REFERENCE: PF544
10 <140> CURRENT APPLICATION NUMBER: US/09/833,118
11 <141> CURRENT FILING DATE: 2001-04-12
13 <150> PRIOR APPLICATION NUMBER: 60/229,358
14 <151> PRIOR FILING DATE: 2000-04-12
16 <150> PRIOR APPLICATION NUMBER: 60/256,931
17 <151> PRIOR FILING DATE: 2000-12-21
18 <150> PRIOR APPLICATION NUMBER: 60/199,384
19 <151> PRIOR FILING DATE: 2000-04-25
20 <160> NUMBER OF SEQ ID NOS: 35
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 23
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <221> NAME/KEY: primer_bind
33 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
35 <400> SEQUENCE: 1
36 cccaagaatt cccttatcca ggc 23
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 33
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <221> NAME/KEY: primer_bind
46 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
48 <400> SEQUENCE: 2
49 gggaagctta gaagccacag gatccctcca cag 33
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 16
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <221> NAME/KEY: misc_structure
59 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
60 with non-cohesive ends.
62 <400> SEQUENCE: 3
63 gataaagatt cccaac 16
66 <210> SEQ ID NO: 4
67 <211> LENGTH: 17
68 <212> TYPE: DNA
69 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:

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72 <221> NAME/KEY: misc_structure
73 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
74     with non-cohesive ends.
76 <400> SEQUENCE: 4
77 aattgttggg aatcttt                                     17
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 17
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <221> NAME/KEY: misc_structure
87 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
88     with non-cohesive ends.
90 <400> SEQUENCE: 5
91 ttaggcttat tccaac                                     17
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 18
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <221> NAME/KEY: misc_structure
101 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
102     with non-cohesive ends.
104 <400> SEQUENCE: 6
105 aattgttggg aataagcc                                     18
108 <210> SEQ ID NO: 7
109 <211> LENGTH: 24
110 <212> TYPE: PRT
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <221> NAME/KEY: SITE
115 <222> LOCATION: 1)..(19)
116 <223> OTHER INFORMATION: invertase leader sequence
118 <220> FEATURE:
119 <221> NAME/KEY: SITE
120 <222> LOCATION: 20)..(24)
121 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
123 <400> SEQUENCE: 7
124 Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
125   1           5           10           15
127 Ile Ser Ala Asp Ala His Lys Ser
128           20
131 <210> SEQ ID NO: 8

```

Artificial Sequence

misc_structure

INFORMATION: synthetic oligonucleotide used to join DNA

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139     fragments with non-cohesive ends.
141 <400> SEQUENCE: 8
142 gagatgcaca cctgagtgag g                                21
145 <210> SEQ ID NO: 9
146 <211> LENGTH: 27
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <221> NAME/KEY: misc_structure
152 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
153     fragments with non-cohesive ends.
155 <400> SEQUENCE: 9
156 gatcctgtgg ctgcgatgca cacaaga                            27
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 24
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <221> NAME/KEY: misc_structure
166 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
167     fragments with non-cohesive ends.
169 <400> SEQUENCE: 10
170 ctcttggtg catcgaagcc acag                                24
173 <210> SEQ ID NO: 11
174 <211> LENGTH: 30
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <221> NAME/KEY: misc_structure
180 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
181     fragments with non-cohesive ends.
183 <400> SEQUENCE: 11
184 tgtggaagag cctcagaatt tattcccaac                        30
187 <210> SEQ ID NO: 12
188 <211> LENGTH: 31
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <221> NAME/KEY: misc_structure
194 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
195     fragments with non-cohesive ends.
197 <400> SEQUENCE: 12
198 aattgttggg aataaattct gaggtcttct c                      31
201 <210> SEQ ID NO: 13
202 <211> LENGTH: 47
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <221> NAME/KEY: misc_structure

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208 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
209     fragments with non-cohesive ends.
211 <400> SEQUENCE: 13
212 ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac          47
215 <210> SEQ ID NO: 14
216 <211> LENGTH: 48
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <221> NAME/KEY: misc_structure
222 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
223     fragments with non-cohesive ends.
225 <400> SEQUENCE: 14
226 aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc          48
229 <210> SEQ ID NO: 15
230 <211> LENGTH: 62
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <221> NAME/KEY: misc_structure
236 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
237     fragments with non-cohesive ends.
239 <400> SEQUENCE: 15
240 ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcggtgg atccttccca 60
241 ac                                                                62
244 <210> SEQ ID NO: 16
245 <211> LENGTH: 63
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <221> NAME/KEY: misc_structure
251 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
252     fragments with non-cohesive ends.
254 <400> SEQUENCE: 16
255 aattgttggg aaggatccac cgccaccaga tccgcgcga ccagatccac caccgcctaa 60
256 gcc                                                                63
259 <210> SEQ ID NO: 17
260 <211> LENGTH: 1782
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
265 <221> NAME/KEY: CDS
266 <222> LOCATION: (1)..(1755)
269 <400> SEQUENCE: 17
270 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa    48
271 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
272   1           5           10           15
274 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag    96
275 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

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```

276          20          25          30
278 cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
279 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
280          35          40          45
282 ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
283 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
284          50          55          60
286 tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
287 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
288 65          70          75          80
290 cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
291 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
292          85          90          95
294 gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
295 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
296          100          105          110
298 ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384
299 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
300          115          120          125
302 gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432
303 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
304          130          135          140
306 aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg 480
307 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
308 145          150          155          160
310 tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc 528
311 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
312          165          170          175
314 tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg 576
315 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
316          180          185          190
318 tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa 624
319 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
320          195          200          205
322 aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc 672
323 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
324          210          215          220
326 aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa 720
327 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
328 225          230          235          240
330 gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac 768
331 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
332          245          250          255
334 agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc 816
335 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
336          260          265          270
338 agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac 864
339 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
340          275          280          285

```

Pleas Note:

Use f n and/ r Xaa hav been detected in the Sequence Listing. Please review the Sequence Listing t ensure that a c rresp nding xplanation is presented in the <220> to <223> fields f each sequence which presents at least ne n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\PF544SL.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:639 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:644 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:654 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:659 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:664 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:674 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:679 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:684 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:689 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:694 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:699 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:704 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:748 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:768 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:773 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:778 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:783 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:817 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:822 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:832 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:837 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:842 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:847 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:852 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:857 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:862 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:872 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:877 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:882 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

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L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:902 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:907 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:912 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:917 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:922 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33